



SEQUENCE LISTING

#12/BB
2/28/01

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FEB 22 2001

TECH CENTER 1600/2900

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Tezuka, Katsunari<120> CELL SURFACE MOLECULE MEDIATING CELL
ADHESION AND SIGNAL TRANSMISSION

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<140> US 09/383,551

<141> 1999-08-26

<150> PCT/JP98/00837

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Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc 144
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat 192
Gln Gln Phe Lys Met Gln Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg 240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta 288
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca 336
 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110

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 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125

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 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140

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 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
 145 150 155 160

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 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
 165 170 175

 aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct 576
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 35 40 45
 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 65 70 75 80
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 85 90 95
 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125
 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
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 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
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gcc	aat	tat	gag	atg	ttt	ata	ttt	cac	aac	gga	ggt	gta	caa	att	tta		148
Ala	Asn	Tyr	Glu	Met	Phe	Ile	Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Leu		
				30					35					40			
tgc	aaa	tat	cct	gac	att	gtc	cag	caa	ttt	aaa	atg	cag	ttg	ctg	aaa		196
Cys	Lys	Tyr	Pro	Asp	Ile	Val	Gln	Gln	Phe	Lys	Met	Gln	Leu	Leu	Lys		
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ggg	ggg	caa	ata	ctc	tgc	gat	ctc	act	aag	aca	aaa	gga	agt	gga	aac		244
Gly	Gly	Gln	Ile	Leu	Cys	Asp	Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn		
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aca	gtg	tcc	att	aag	agt	ctg	aaa	ttc	tgc	cat	tct	cag	tta	tcc	aac		292
Thr	Val	Ser	Ile	Lys	Ser	Leu	Lys	Phe	Cys	His	Ser	Gln	Leu	Ser	Asn		
	75					80					85						
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Asn	Ser	Val	Ser	Phe	Phe	Leu	Tyr	Asn	Leu	Asp	His	Ser	His	Ala	Asn		
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Tyr	Tyr	Phe	Cys	Asn	Leu	Ser	Ile	Phe	Asp	Pro	Pro	Pro	Phe	Lys	Val		
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Thr	Leu	Thr	Gly	Gly	Tyr	Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys		
			125					130					135				
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Gln	Leu	Lys	Phe	Trp	Leu	Pro	Ile	Gly	Cys	Ala	Ala	Phe	Val	Val	Val		
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190 195

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Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Asn	
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gac	ttg	gcc	aat	cac	agg	atg	ttt	tcg	ttt	cac	gat	gga	ggg	gta	cag	151
Asp	Leu	Ala	Asn	His	Arg	Met	Phe	Ser	Phe	His	Asp	Gly	Gly	Val	Gln	
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att	tct	tgt	aac	tac	cct	gag	act	gtc	cag	cag	tta	aaa	atg	cag	ttg	199
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gccctggcac	tttaagatag	ccttcttttag	aacatgagtt	agttggtagt	attctgacgt	1944
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Leu	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	Ala	Asp	His	Arg	Met	Phe	Ser	
			20					25						30		

ttt	cac	aat	gga	ggg	gta	cag	att	tct	tgt	aaa	tac	cct	gag	act	gtc	144
Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val	
		35					40					45				

cag	cag	tta	aaa	atg	cga	ttg	ttc	aga	gag	aga	gaa	gtc	ctc	tgc	gaa	192
Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu	
		50				55					60					

ctc	acc	aag	acc	aag	gga	agc	gga	aat	gcg	gtg	tcc	atc	aag	aat	cca	240
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro	
65					70					75					80	

atg	ctc	tgt	cta	tat	cat	ctg	tca	aac	aac	agc	gtc	tct	ttt	ttc	cta	288
Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu	
				85					90					95		

aac	aac	cca	gac	agc	tcc	cag	gga	agc	tat	tac	ttc	tgc	agc	ctg	tcc	336
Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser	
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Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr	
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ttg	cat	att	tat	gaa	tcc	cag	ctc	tgc	tgc	cag	ctg	aag	ctc	tgg	cta	432
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu	
		130				135					140					

ccc	gta	ggg	ttg	cca	gct	ttc	gtt	gtg	gta	ctc	ctt	ttt	gga	tgc	ata	480
Pro	Val	Gly	Leu	Pro	Ala	Phe	Val	Val	Val	Leu	Leu	Phe	Gly	Cys	Ile	
145					150					155				160		

ctt	atc	atc	tgg	ttt	tca	aaa	aag	aaa	tac	gga	tcc	agt	gtg	cat	gac	528
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Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe			
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Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Thr Ala			
185	190	195	
ccc ctt agg gct ttg ggg aga gga gaa cac tct tca tgt caa gac cgg			679
Pro Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg			
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Asn			
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Gln Ile Ser Cys Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
35 40 45
Phe Lys Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly
50 55 60
Asn Thr Val Ser Ile Lys Asn Pro Met Cys Tyr Gln Leu Ser Asn Asn
65 70 75 80
Ser Val Ser Phe Phe Leu Asn Asp Ser Ser Gln Gly Ser Tyr Cys Ser
85 90 95
Leu Ser Ile Phe Asp Pro Pro Pro Phe Gln Glu Asn Leu Ser Gly Gly
100 105 110
Tyr Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
115 120 125
Pro Val Gly Cys Ala Ala Phe Val Leu Leu Phe Gly Cys Ile Ile Trp
130 135 140
Phe Lys Lys Lys Tyr Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met
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Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
      35           40           45
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
      50           55           60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65           70           75           80
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
      85           90           95
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
      100          105          110
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
      115          120          125
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
      130          135          140
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145          150          155          160
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
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Arg Leu Thr Asp Val Thr Leu
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Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
      50           55           60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65           70           75           80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
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Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
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Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
      115          120          125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
      130          135          140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145          150          155          160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
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Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
      180          185          190
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro

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 50 55 60
 Lys Ala Tyr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
 65 70 75 80
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 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
 100 105 110
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
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 Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
 130 135 140
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 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175
 Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190
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 Leu Gln Asn Leu Thr Tyr Phe Cys Lys Glu Met Tyr Pro Pro Pro Tyr
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 Asn Gly Thr Ile His Val Leu Cys Pro Phe Trp Leu Val Leu Tyr Ser
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 Leu Thr Ala Ile Lys Lys Arg Ser Leu Gly Tyr Met Met Pro Pro Lys
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 Gln Pro Tyr Asp Phe

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 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val

[illegible]